

```

1 MRENMARGPCNAPRWVSLMVLVAIGTAVTA AVNPGVVVRISQKGLDYASQ 50
  |||||
1 MRENMARGPCNAPRWVSLMVLVAIGTAVTA AVNPGVVVRISQKGLDYASQ 50

51 QGTAALQKELKRIKIPDYSDFEIKHLGKGHYSFYSMDIREFQLPSSQIS 100
  |||||
51 QGTAALQKELKRIKIPDYSDFEIKHLGKGHYSFYSMDIREFQLPSSQIS 100

1101 MVPNVGLKFESISNANIKISGKWKAQKRFKMGSGNFDLSIEGMSISADLKL 150
  |||||
1101 MVPNVGLKFESISNANIKISGKWKAQKRFKMGSGNFDLSIEGMSISADLKL 150

151 GSNPTSGKPTTTCSSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNK 200
  |||||
151 GSNPTSGKPTTTCSSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNK 200

201 MNSQVCEKVTNSVSSKLQPYFQTLPMVTKIDSVAGINYGLVAPPATTAET 250
  |||||
201 MNSQVCEKVTNSVSSKLQPYFQTLPMVTKIDSVAGINYGLVAPPATTAET 250

```

Fig. 1

251 LDVQMKGEFYSENHHNPPPPFAPPVMEFFPAAHDMVYLGSLDYFFENTAGLV 300
|||||
251 LDVQMKGEFYSENHHNPPPPFAPPVMEFFPAAHDMVYLGSLDYFFENTAGLV 300
|||||
301 YQEAGVLKMTLRDDMIPKESKERLTTKFFGTFLPEVAKKFPNMKIQIHVS 350
|||||
301 YQEAGVLKMTLRDDMIPKESKERLTTKFFGTFLPEVAKKFPNMKIQIHVS 350
|||||
351 ASTPPHLSVQPTGLTFYPADVQAFVLPNSSLASLFLIGM 391
|||||
351 ASTPPHLSVQPTGLTFYPADVQAFVLPNSSLASLFLIGM 391

Fig. 1 (Cont.)

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1 MGRQLVLVLGLTCCWAVASAAKLGAVYTEGGFVEGVNKKLGLLGDSVDIF 50
|||||
1 MGRQLVLVLGLTCCWAVASAAKLGAVYTEGGFVEGVNKKLGLLGDSVDIF 50
51 KGIPFAAPTCALENPQHPGWQGTCLKAKNFKKRCLOATITQDSTYGDEDC 100
|||||
51 KGIPFAAPTCALENPQHPGWQGTCLKAKNFKKRCLOATITQDSTYGDEDC 100
101 LYLNIWVPQGRKQVSRDLPVMIWIYGGAFIMGSGHGANFLNNLYDGEI 150
|||||
101 LYLNIWVPQGRKQVSRDLPVMIWIYGGAFIMGSGHGANFLNNLYDGEI 150
151 ATRGNVIVVTENYRVGPLGFLSTGDANLPGNYGLRDQHMAIAWVKRNIAA 200
|||||
151 ATRGNVIVVTENYRVGPLGFLSTGDANLPGNYGLRDQHMAIAWVKRNIAA 200
201 FGGDPNNITLFGESAGGASVSLQTLSPYNKGLIRRAISQSGVALSPWVIQ 250
|||||
201 FGGDPNNITLFGESAGGASVSLQTLSPYNKGLIRRAISQSGVALSPWVIQ 250

Fig. 2

251 KNPLFWAKKVAEKVGCPCVGDAAARMAQCLKVTDPRALTLAYKVPLAGLEYP 300
|||||
251 KNPLFWAKKVAEKVGCPCVGDAAARMAQCLKVTDPRALTLAYKVPLAGLEYP 300

301 MLHYVGFVPVIDGDFIPADPINLYANAADIDYIAGTNNMDGHIFASIDMP 350
|||||
301 MLHYVGFVPVIDGDFIPADPINLYANAADIDYIAGTNNMDGHIFASIDMP 350

351 AINKGNKKVTEEDFYKLVSEFTITKGLRGAKTTFDVYTESWAQDPSQENK 400
|||||
351 AINKGNKKVTEEDFYKLVSEFTITKGLRGAKTTFDVYTESWAQDPSQENK 400

401 KKTVVDFETDVLFLVPTETIALAQHRANAKSAKTYAYLFESHPSRMPVYPKW 450
|||||
401 KKTVVDFETDVLFLVPTETIALAQHRANAKSAKTYAYLFESHPSRMPVYPKW 450

451 VGADHADDIQYVFGKPFATPTGYRPODRTVSKAMIAYTWNFAKTGDPNMG 500
|||||
451 VGADHADDIQYVFGKPFATPTGYRPODRTVSKAMIAYTWNFAKTGDPNMG 500

Fig. 2 (Cont.)

501 DSAVPTHWEPTYTTENSGYLEITKKMGSSSMKRSLRTNFLRYWTLTYLALP 550
|||||
501 DSAVPTHWEPTYTTENSGYLEITKKMGSSSMKRSLRTNFLRYWTLTYLALP 550
551 TVTDQEATVPVPPPTGDSSEATVPVPPPTGDSSEATVPVPPPTGDSGAPPVPPPTGDSG 600
|||||
551 TVTDQEATVPVPPPTGDSSEATVPVPPPTGDSSEATVPVPPPTGDSGAPPVPPPTGDSG 600
601 APPVPPPTGDSGAPPVPPPTGDSSEA 623
|||||
601 APPVPPPTGDSGAPPVPPPTGDSGA 623

Fig. 2 (Cont.)

Fig. 3

Fig. 3

251 QARNWGLGGHAFCRNPNDNDIRPWCFLNDRDRLSWEYCDLAQCQTPTQAAP 300
 |||||
 254 QARNWGLGGHAFCRNPNDNDIRPWCFLNDRDRLSWEYCDLAQCQTPTQAAP 303
 |||||
 301 PTPVSPRLHVPLMPAQAPPKPQPTTRTPPQSQTTPGALPAKREQPPSLTR 350
 |||||
 304 PTPVSPRLHVPLMPAQAPPKPQPTTRTPPQSQTTPGALPAKREQPPSLTR 353
 |||||
 351 NGPLSCGQRLRKSLSSMTRVVGGVALRGAHPYIAALYWGHSTFCAGSLIA 400
 |||||
 354 NGPLSCGQRLRKSLSSMTRVVGGVALRGAHPYIAALYWGHSTFCAGSLIA 403
 |||||
 401 PCWVLTAAHCLQDRPAPEDLTVVLGQERRNHSCEPCQTLAVRSYRLHEAF 450
 |||||
 404 PCWVLTAAHCLQDRPAPEDLTVVLGQERRNHSCEPCQTLAVRSYRLHEAF 453
 |||||
 451 SPVSYQHDLALLRLQEDADGSCALLSPYVQPVCLPSGAARPSETTLCQVA 500
 |||||
 454 SPVSYQHDLALLRLQEDADGSCALLSPYVQPVCLPSGAARPSETTLCQVA 503
 |||||

Fig. 3 (Cont.)

501 GWGHQFEAEYASFLQEAQVPFLSLERCSAPDVHGSSILPGMLCAGFLE 550
 |||||
 504 GWGHQFEAEYASFLQEAQVPFLSLERCSAPDVHGSSILPGMLCAGFLE 553
 |||||
 551 GGTDACAGELLAGWRPSRPSAXSQVHSADCVFPTQGDGGPLVCEDQAA 600
 |||||
 554 GGTDAC.....QGDSGGPLVCEDQAA 574
 601 ERRLTQGIISWGSGCCDRNKPQVYTDVAYYLAWIREHTVS 641
 |||||
 575 ERRLTQGIISWGSGCCDRNKPQVYTDVAYYLAWIREHTVS 615

Fig. 3 (Cont.)


```

1 MAPFEPLASGILLLLWLIAPSRACCTVPPHPQTAFNCNSDLVIRAKFVGTP 50
|||||
51 EVNQTTLYQRYEIKMTKMYKGFQALGDAADIREFVYTPAMESVCGYFHRSH 100
|||||
51 EVNQTTLYQRYEIKMTKMYKGFQALGDAADIREFVYTPAMESVCGYFHRSH 150
|||||
101 NRSEEFLLIAGKLQDGLLHITTCSEFVAPWNLSLAQRRGFTKTYTVGCEE 150
|||||
101 NRSEEFLLIAGKLQDGLLHITTCSEFVAPWNLSLAQRRGFTKTYTVGCEE 150
|||||
151 TVEPC 155
151 TVEPC 155

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Fig. 4

```

1 MAPFEPLASGILLLWLIAPSRACCTCVPPHPQTAFNCSDLVIRAKFVGTP 50
  |||||
1 MAPFEPLASGILLLWLIAPSRACCTCVPPHPQTAFNCSDLVIRAKFVGTP 50

51 EVNQTTLYQRYEIKMTKMYKGFOALGDAADIRFVYTPAMESVCGYFHRSH 100
  |||||
51 EVNQTTLYQRYEIKMTKMYKGFOALGDAADIRFVYTPAMESVCGYFHRSH 100

      101 NRSEEFLLIAGKLQ 113
        |||||
      101 NRSEEFLLIAGKLQ 113

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Fig. 5

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1  MAPFEPLASGILLLLWLIAPSRACCTCVPPHPQTAFCNSSLVIRAKFVGTP 50
   |||||
1  MAPFEPLASGILLLLWLIAPSRACCTCVPPHPQTAFCNSSLVIRAKFVGTP 50
   |||||
51 EVNQTTLYQRYEIKMTKMYKGFGALGDAADIRFVYTPAMESVCGYFHRSH 100
   |||||
51 EVNQTTLYQRYEIKMTKMYKGFGALGDAADIRFVYTPAMESVCGYFHRSH 100
   |||||
101 NRSEEFLLI..... 108
     |||||
101 NRSEEFLLIAGKLQDGLLHITTCSFVAPWNLSLAQRGRFTKTYTVGCEE 150
   |||||
109 .....LSIPCKLQSGTHCLWTDQLLQSEKGFQSRHLACLPREPGLCTWQ 153
     |||||
151 TVFPCLIPCKLQSGTHCLWTDQLLQSEKGFQSRHLACLPREPGLCTWQ 200
     |||||
154 SLRSQIA 160
     |||||
201 SLRSQIA 207

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Fig. 7

1 MAPFEPLASGILLLLWLIAPSRACVPPHPQTAFNCNSDLVIRAKFVGTP 50
|||||
1 MAPFEPLASGILLLLWLIAPSRACVPPHPQTAFNCNSDLVIRAKFVGTP 50
51 EVNQTTLYQRYEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHR... 98
|||||
51 EVNQTTLYQRYEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSH 100
99AGKLQDGLLHITTCSFVAPWNSLSLAQRRGFTKTYTVGCCEC 140
|||||
101 NRSEEFIAAGKLQDGLLHITTCSFVAPWNSLSLAQRRGFTKTYTVGCCEC 150
141 TVFPCLSI PCKLQSGTHCLWTDQLQSEKGFQSRHLACLPREPGLCTWQ 190
|||||
151 TVFPCLSI PCKLQSGTHCLWTDQLQSEKGFQSRHLACLPREPGLCTWQ 200
191 SLRSQIA 197
|||||
201 SLRSQIA 207

Fig. 8

1 MRALLARLLLCVWSDSKGSNELHQVPSNCDCLNGGTCVSNKYFSNIHW 50
|||||
1 MRALLARLLLCVWSDSKGSNELHQVPSNCDCLNGGTCVSNKYFSNIHW 50
51 CNCPKKEGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVL 100
|||||
51 CNCPKKEGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVL 100
101 QQTYHAHRSDALQLGLGKHNYCREVGAQGPKALPTVPRNLVTIPFSQRAG 150
|||||
101 QQTYHAHRSDALQLGLGKHNYCR..... 123
151 HSTREVQPLVESSLRGGGREGPLGWNDIPYLSVLPGNPDNRRRPWCYVQV 200
|||||
124NPDNRRRPWCYVQV 137
201 GLKPLVQECMVHDCADGKKPSSPPEELKFQCGQKTLRPRFKIIGGEFTTI 250
|||||
138 GLKPLVQECMVHDWADGKKPSSPPEELKFQCGQKTLRPRFKIIGGEFTTI 187

Fig. 9

251 ENQWFAAIYRRHGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIV 300
 |||||
 188 ENQWFAAIYRRHGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIV 350
 |||||
 301 YLGRSRLNSNTQGMKFEVENLILHKDYSADTLAHNDIALLKIRSKETR 287
 |||||
 238 YLGRSRLNSNTQGMKFEVENLILHKDYSADTLAHNDIALLKIRSKETR 400
 |||||
 351 CAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVV 337
 |||||
 288 CAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKENSTDYLYPEQLKMTVV 450
 |||||
 401 KLISHRECQPHYGYSEVTKMLCAADPQWKTDSCQGDGGPLVCSLQCR 387
 |||||
 338 KLISHRECQPHYGYSEVTKMLCAADPQWKTDSCQGDGGPLVCSLQCR 494
 |||||
 451 MTLTGIVSWGRCALKDKPGVYTRVSHFLPWIRSHTEENGLAL 431
 |||||
 388 MTLTGIVSWGRCALKDKPGVYTRVSHFLPWIRSHTEENGLAL 431

Fig. 9 (Cont.)

1 MQMSPALTCLVLGLALVFEGESAVHHPPSYVAHLASDEGVRVFQQVAQAS 50
|||||
1 MQMSPALTCLVLGLALVFEGESAVHHPPSYVAHLASDEGVRVFQQVAQAS 50
51 KDRNVVFSPYGVASVLAMLQLTTGGETQQQIQAAAMGFKIDDKGMAPALRH 100
|||||
51 KDRNVVFSPYGVASVLAMLQLTTGGETQQQIQAAAMGFKIDDKGMAPALRH 100
101 LYKELMGPWNKDEISTDAIFVQORDLKLVOGFMPHFRLFRSTVVKQVDFS 150
|||||
101 LYKELMGPWNKDEISTDAIFVQORDLKLVOGFMPHFRLFRSTVVKQVDFS 150
151 EVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKT 200
|||||
151 EVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKT 200
201 PFPDSSTHRRLEFHKS DGS TVSVPMMAQTNKFNYTEFTTPDGHYYDILELP 250
|||||
201 PFPDSSTHRRLEFHKS DGS TVSVPMMAQTNKFNYTEFTTPDGHYYDILELP 250
251 YHGD T L S M F I A A D L . . . V P T E A L 270
|||||
251 YHGD T L S M F I A A P Y E K E V P L S A L 273

Fig. 10

Fig. 11

Fig. 11 (Cont.)

Fig. 12

Fig. 12

169 VQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENI 218
|||||
201 VQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENI 250
|||||
219 KKGKKCIRTPKISKPIKFEELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTT 268
|||||
251 KKGKKCIRTPKISKPIKFEELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTT 300
|||||
269 LPVEFKCPDGEVMKKNNMFIKTCACHYNCPGDNDIFESLYRKMYGDMA 317
|||||
301 LPVEFKCPDGEVMKKNNMFIKTCACHYNCPGDNDIFESLYRKMYGDMA 349
|||||

Fig. 12 (Cont.)

Fig. 13

253 AIEGKDAVLECCVSGYPPPSFTWLRGEEVIQLRSKKYSLGGSNLLISNV 302
|||||
251 AIEGKDAVLECCVSGYPPPSFTWLRGEEVIQLRSKKYSLGGSNLLISNV 300
303 TDDDSGMYTCVVVTKNENISASAELTVLV 331
|||||
301 TDDDSGMYTCVVVTKNENISASAELTVLV 329

Fig. 13 (Cont.)

3 MENSIRCVWVPKLAFLVLFASLLSAHLQVTGFQIKAFALRFLSEPSDAV 52
|||||
1 MENSIRCVWVPKLAFLVLFASLLSAHLQVTGFQIKAFALRFLSEPSDAV 50
53 TMRGGNVLLDCSAESDRGVPVIKWKDAIHLALGMDERKQQLSNGSLLIQ 102
|||||
51 TMRGGNVLLDCSAESDRGVPVIKWKDGIHLALGMDERKQQLSNGSLLIQ 100
103 NILHSRHHKPDDEGLYQCEASLGDSGSIISRTAKVAVAGPLRFLSQTESVT 152
|||||
101 NILHSRHHKPDDEGLYQCEASLGDSGSIISRTAKVAVAGPLRFLSQTESVT 150
153 AFMGDTVLLKCEVIGEPMTIHWQKNQODLTPIPGDSRVVVLPSGALQIS 202
|||||
151 AFMGDTVLLKCEVIGEPMTIHWQKNQODLTPIPGDSRVVVLPSGALQIS 200
203 RLQPGDIGIYRCSARNPASSRTGNEAEVRILSDPGLHRQLYFLQRPNSVV 252
|||||
201 RLQPGDIGIYRCSARNPASSRTGNEAEVRILSDPGLHRQLYFLQRPNSVV 250
253 AIEGKDAVLECCVSGYPPPSFTWLRGEEVIQLRSKKYSLGGSNLLISNV 302
|||||
251 AIEGKDAVLECCVSGYPPPSFTWLRGEEVIQLRSKKYSLGGSNLLISNV 300

Fig. 14

303 TDDDSGMYTCVVTYKNENISASAELTVLPFWFLNHPNSNLAYESMDIEF 352
 |||||
 301 TDDDSGMYTCVVTYKNENISASAELTVLPFWFLNHPNSNLAYESMDIEF 350
 |||||
 353 ECTVSGKPVPTVNMKNGDVVIPSDFQIVGGSNLRILGVVKSDEGFYQC 402
 |||||
 351 ECTVSGKPVPTVNMKNGDVVIPSDFQIVGGSNLRILGVVKSDEGFYQC 400
 |||||
 403 VAENEAGNAQTSACLIVPKPAIPSSSVLPSAPRDVVPVLVSSRFVRLSWR 452
 |||||
 401 VAENEAGNAQTSACLIVPKPAIPSSSVLPSAPRDVVPVLVSSRFVRLSWR 450
 |||||
 453 PPAEAKGNIQTFTVFFSREGDNRRERALNTTQPGSLQLTVGNLKPEAMYTF 502
 |||||
 451 PPAEAKGNIQTFTVFFSREGDNRRERALNTTQPGSLQLTVGNLKPEAMYTF 500
 |||||
 503 RVVAYNEWGPGESSQPIKVATOPELQVPGPVENLQAVSTSPSTSLITWEP 552
 |||||
 501 RVVAYNEWGPGESSQPIKVATOPELQVPGPVENLQAVSTSPSTSLITWEP 550
 |||||
 553 PAYANGPVQGYRLFCFTEVSTGKEQNIQVVDGLSYKLEGLKKFTEYSIRFLA 602
 |||||
 551 PAYANGPVQGYRLFCFTEVSTGKEQNIQVVDGLSYKLEGLKKFTEYSIRFLA 600
 |||||

Fig. 14 (Cont.)

603	YNRYGPGVSTDDITVVTLS	VDVPSAPPQNV	SLFVVNSRSIKVSWLPP	PSGT	652
601	YNRYGPGVSTDDITVVTLS	VDVPSAPPQNV	SLFVVNSRSIKVSWLPP	PSGT	650
653	QNGFITGYKIRHRKTT	RRGEMETLEPN	NLWYLETGLEKGSQ	YSFQVSAMT	702
651	QNGFITGYKIRHRKTT	RRGEMETLEPN	NLWYLETGLEKGSQ	YSFQVSAMT	700
703	VNGTGPPSNWYTAET	PENDLDESQVDP	QSSLHVRPQTNCI	IMSWTPPLN	752
701	VNGTGPPSNWYTAET	PENDLDESQVDP	QSSLHVRPQTNCI	IMSWTPPLN	750
753	PNIVVRGYIIGYGV	CSPYAETVRVDS	KQRYYSIERLESS	SHYVISLKAEN	802
751	PNIVVRGYIIGYGV	CSPYAETVRVDS	KQRYYSIERLESS	SHYVISLKAEN	800
803	NAGECVPLYESAT	TRSDPTDPVDY	YPLDDFPTSV	PDLSTPMLPPGV	852
801	NAGECVPLYESAT	TRSDPTDPVDY	YPLDDFPTSV	PDLSTPMLPPGV	850
853	QAVALTHDAVRV	SWADNSVPKNQKT	SEVRLYTVRWRTS	FSASAKYKSEDT	902
851	QAVALTHDAVRV	SWADNSVPKNQKT	SEVRLYTVRWRTS	FSASAKYKSEDT	900

Fig. 14 (Cont.)

903 TSLSYTATGLKPNMTMYEFSVMVTKNRRSSTWSMTAHATTYEAAPTAPKD 952
|||||
901 TSLSYTATGLKPNMTMYEFSVMVTKNRRSSTWSMTAHATTYEAAPTAPKD 950

953 FTVITREGKPRAVIVSWQPPLEANGKITAYILFYTLDKNIPIDDWIMETI 1002
|||||
951 FTVITREGKPRAVIVSWQPPLEANGKITAYILFYTLDKNIPIDDWIMETI 1000

1003 SGDRLTHQIMDLNLDTMYFYRIQARNKSGVGPLSDPILFRTLKVEHPDKM 1052
|||||
1001 SGDRLTHQIMDLNLDTMYFYRIQARNKSGVGPLSDPILFRTLKVEHPDKM 1050

1053 ANDQGRHGDGGYWPVDTNLIDRSTLNEPPIGQMHPHSGVTPQKNSNLLV 1102
|||||
1051 ANDQGRHGDGGYWPVDTNLIDRSTLNEPPIGQMHPHSGVTPQKNSNLLV 1100

1103 IIVVTVGVIITVLVVIVAVICTRRSSAQQRKKRATHSAGKRKGSQKDLRP 1152
|||||
1101 IIVVTVGVIITVLVVIVAVICTRRSSAQQRKKRATHSAGKRKGSQKDLRP 1150

1153 PDLWIHHEEMEMKNI EKPSGTD PAGRDSPIQSCQDLTPVSHSQSETQLGS 1202
|||||
1151 PDLWIHHEEMEMKNI EKPSGTD PAGRDSPIQSCQDLTPVSHSQSETQLGS 1200

Fig. 14 (Cont.)

1203 KSTSHSGQDTEEEAGSSMSTLERSLAARRAPRAKLMIPMDAQSNPPAVVSA 1252
|||||
1201 KSTSHSGQDTEEEAGSSMSTLERSLAARRAPRAKLMIPMDAQSNPPAVVSA 1250
|||||
1253 IPVPTLESAQYPGILPSPTCGYPHPQFTLRPVPEPTLSVDRGEFAGRSQS 1302
|||||
1251 IPVPTLESAQYPGILPSPTCGYPHPQFTLRPVPEPTLSVDRGEFAGRSQS 1300
|||||
1303 VSEGPTTQQPPMLPPSQPEHSSSEEEAPSRPTIPTACVRPTHPLRSFANPLL 1352
|||||
1301 VSEGPTTQQPPMLPPSQPEHSSSEEEAPSRPTIPTACVRPTHPLRSFANPLL 1350
|||||
1353 PPPMSAIEPKVPYTPLLSQPGPTLPKTHVKTASLGLAGKARSPLLPVSV 1402
|||||
1351 PPPMSAIEPKVPYTPLLSQPGPTLPKTHVKTASLGLAGKARSPLLPVSV 1400
|||||
1403 TAPEVSEESHKPTEDSANV 1421
|||||
1401 TAPEVSEESHKPTEDSANV 1419

Fig. 14 (Cont.)

1 MPGKRGWGWWARLPLCLLLSLYGPWMPSSLGKPKGHPHMNSIRIDGIT 50
|||||
1 MPGKRGWGWWARLPLCLLLSLYGPWMPSSLGKPKGHPHMNSIRIDGIT 50

51 LGGLEFPVHGRGSEKPCGELKKKEKGIHRLLEAMLFALDRINNDPDLNIT 100
|||||
51 LGGLEFPVHGRGSEKPCGELKKKEKGIHRLLEAMLFALDRINNDPDLNIT 100

101 LGARILDTCSRDTHALEQSLTFVQALIEKDGTEVRCGSGGPPITTKPERV 150
|||||
101 LGARILDTCSRDTHALEQSLTFVQALIEKDGTEVRCGSGGPPITTKPERV 150

151 VGVIGASGSSVSIMVANILRLFKIPQISYASTAPDLSNDRYDFFSRVVP 200
|||||
151 VGVIGASGSSVSIMVANILRLFKIPQISYASTAPDLSNDRYDFFSRVVP 200

201 SDTYQAQAMVDIVRAKWNVSTVASEGSYGESGVEAFIQKSREDGGVCI 250
|||||
201 SDTYQAQAMVDIVRAKWNVSTVASEGSYGESGVEAFIQKSREDGGVCI 250

251 AQS VKIPREP KAGEFDKIIRRLLET SNARAVIIFANEDDIRRVLEAARRA 300
|||||
251 AQS VKIPREP KAGEFDKIIRRLLET SNARAVIIFANEDDIRRVLEAARRA 300

Fig. 15

```

301 NQTGHFFWMSGDSWGSKIAPVLHLEEVAEGAVTILPKRMSVR..... 342
    |||||
301 NQTGHFFWMSGDSWGSKIAPVLHLEEVAEGAVTILPKRMSVRGFDRYESS 350

343 .....DRERIGQDSAY 353
    .|||||

351 RTLDNNRRNIWFAEFWEDNEHCKLSRHALKKGSHVKKCTNRERIGQDSAY 400

354 EQEGKVQFVIDAVYAMGHALHAMHRDLCPRVGLCPRMDPVDGTQLLKYI 403
    |||||
401 EQEGKVQFVIDAVYAMGHALHAMHRDLCPRVGLCPRMDPVDGTQLLKYI 450

404 RNVNFSGIAGNPVTFNENGDAPEGRIYQYQLRNDSEYKVIGSWTDHLH 453
    |||||
451 RNVNFSGIAGNPVTFNENGDAPEGRIYQYQLRNDSEYKVIGSWTDHLH 500

454 LRIERMHWPGSGQQLPRSLPCQPGERKKTVKGMPCWHCEPCTGYQY 503
    |||||
501 LRIERMHWPGSGQQLPRSLPCQPGERKKTVKGMPCWHCEPCTGYQY 550

504 QVDRYTCKTCPYDMRPTENRTGCRPIPIKLEWGSPWAVLPLFLAVVGIA 553
    |||||
551 QVDRYTCKTCPYDMRPTENRTGCRPIPIKLEWGSPWAVLPLFLAVVGIA 600

```

Fig. 15 (Cont.)

554 ATLFVITFVRYNDTPIVKASGRELSYVLLAGIFLCYATTFMLIAEPDLG 603
|||||
601 ATLFVITFVRYNDTPIVKASGRELSYVLLAGIFLCYATTFMLIAEPDLG 650
|||||
604 TC SLRRIFLGLGMSISYAALLTKTNRIYRIFEQGRSVSAPRFISPASQL 653
|||||
651 TC SLRRIFLGLGMSISYAALLTKTNRIYRIFEQGRSVSAPRFISPASQL 700
|||||
654 AITFSLISLQLLGICVWFVVDPSHSVDFQDQRTLDPRFARGVLKCDISD 703
|||||
701 AITFSLISLQLLGICVWFVVDPSHSVDFQDQRTLDPRFARGVLKCDISD 750
|||||
704 LSLICLLGYSM LLMVTCTVYAIKTRGVPETENEAKPIGFTMYTTCIVWLA 753
|||||
751 LSLICLLGYSM LLMVTCTVYAIKTRGVPETENEAKPIGFTMYTTCIVWLA 800

Fig. 15 (Cont.)

754 FIPIFFGTSQSADKLYIQTTTLTVSVLSASVSLGMLYMPKVYIILFHPE 803
|||||
801 FIPIFFGTSQSADKLYIQTTTLTVSVSVLSASVSLGMLYMPKVYIILFHPE 850

804 QNVPKRKRSLKAVVTAATMSNKFTQKGNFRPNGEAKSELCEALEAPALAT 853
|||||
851 QNVPKRKRSLKAVVTAATMSNKFTQKGNFRPNGEAKSELCEALEAPALAT 900

854 KQTYVTTYTNHAI 865
|||||
901 KQTYVTTYTNHAI 912

Fig. 15 (Cont.)

Fig. 16


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301 ANINNSRCSVSSPSNTNRRSTLSSPAASTVGSICSPVNNAFSYTASG TSA 350
|||||
301 ANINNSRCSVSSPSNTNRRSTLSSPAASTVGSICSPVNNAFSYTASG TSA 350

351 GSSTLRDVVPSPDTQEKGAQEVFPFKTEEVESAISNGVTGQLNIVQYIKP 400
|||||
351 GSSTLRDVVPSPDTQEKGAQEVFPFKTEEVESAISNGVTGQLNIVQYIKP 400

401 EPDGAFFSSCLGNSKINSDSSFSVPIKQESTKHSCSGTSFKGNPTVNP F 450
|||||
401 EPDGAFFSSCLGNSKINSDSSFSVPIKQESTKHSCSGTSFKGNPTVNP F 450

451 PFMDGSYFSEFMDDKDYSLSGILGPPVPGFDGNCEGSGFPVGIKQEPDDG 500
|||||
451 PFMDGSYFSEFMDDKDYSLSGILGPPVPGFDGNCEGSGFPVGIKQEPDDG 500

501 SYYPEASIPSSAIVGVNSGGQSFHYRIGAQGTISLSRSARDQSFQHLSSF 550
|||||
501 SYYPEASIPSSAIVGVNSGGQSFHYRIGAQGTISLSRSARDQSFQHLSSF 550

551 PPVNTLVESWKSHGDLSSRRSDGYPVLEYIPENVSSSTLRSVSTGSSRRPS 600
|||||
551 PPVNTLVESWKSHGDLSSRRSDGYPVLEYIPENVSSSTLRSVSTGSSRRPS 600

```

Fig. 16 (Cont.)

Fig. 16 (Cont.)

1 METKGYHSLPEGLDMERRWGQVSQAVERSLGPTERTDENNYMEIVNVSC 50
|||||
1 METKGYHSLPEGLDMERRWGQVSQAVERSLGPTERTDENNYMEIVNVSC 50

51 VSGAIPNNSTQGSKEKEQELLPCLOQDNNRPGILTSDIKTELESKELSAT 100
|||||
51 VSGAIPNNSTQGSKEKEQELLPCLOQDNNRPGILTSDIKTELESKELSAT 100

101 VAESMGLYMDSVRDADYSYEQQNQQGSMSPAKIYQNVQVEQLVKFYKGNHR 150
|||||
101 VAESMGLYMDSVRDADYSYEQQNQQGSMSPAKIYQNVQVEQLVKFYKGNHR 150

151 PSTLSCVNTPLRSEMSDSSVNGGVMRAIVKSPIMCHEKSPSVCPLNM 200
|||||
151 PSTLSCVNTPLRSEMSDSSVNGGVMRAIVKSPIMCHEKSPSVCPLNM 200

201 TSSVCSPAGINSVSSTTASFGSPVHSPITQGTPLTCSPPAENRGRSHS 250
|||||
201 TSSVCSPAGINSVSSTTASFGSPVHSPITQGTPLTCSPPAENRGRSHS 250

251 PAHASNVGSPLSPLSSMKSSISSPPSHCSVKSPVSSPNNVTLRSSVSSP 300
|||||
251 PAHASNVGSPLSPLSSMKSSISSPPSHCSVKSPVSSPNNVTLRSSVSSP 300

Fig. 17

301 ANINNSRCVSSPSNTNRRSTLSSPAASTVGSICSPVNNAFSYTAGTSA 350
|||||
301 ANINNSRCVSSPSNTNRRSTLSSPAASTVGSICSPVNNAFSYTAGTSA 350
351 GSSTLRDVVPSPDTOEKGAQEVFPFKTEEVESAISNGVTGQLNIVQYIKP 400
|||||
351 GSSTLRDVVPSPDTOEKGAQEVFPFKTEEVESAISNGVTGQLNIVQYIKP 400
401 EPDGAFFSSCLGNSKINSDDSSFSVPIKQESTKHSCSGTSFKGNPTVNP 450
|||||
401 EPDGAFFSSCLGNSKINSDDSSFSVPIKQESTKHSCSGTSFKGNPTVNP 450
451 PFMDGSYFSEFMDKDYYSLSGILPPVPGFDGNCESGFPVGIKQEPDDG 500
|||||
451 PFMDGSYFSEFMDKDYYSLSGILPPVPGFDGNCESGFPVGIKQEPDDG 500
501 SYYPEASIPSSAIVGVNSGGQSFHYRIGAQTISLSRSARDQSFQHLSSF 550
|||||
501 SYYPEASIPSSAIVGVNSGGQSFHYRIGAQTISLSRSARDQSFQHLSSF 550
551 PPVNTLVESWKSHGDLSSRRSDGYPVLEYIPENVSSSLRSVSTGSSRPS 600
|||||
551 PPVNTLVESWKSHGDLSSRRSDGYPVLEYIPENVSSSLRSVSTGSSRPS 600

Fig. 17 (Cont.)

Fig. 17 (Cont.)

```

1  MGRQLVVLGLTCCWAVASAAKLGAVYTEGGFVEGVNKKLGLLGDSDVDF 50
   |||||
1  MGRQLVVLGLTCCWAVASAAKLGAVYTEGGFVEGVNKKLGLLGDSDVDF 50

51  KGIPFAAPTCALENPQPHPGWQGTCLKAKNEFKKRCQLQATITQDSTYGDEDC 100
   |||||
51  KGIPFAAPTCALENPQPHPGWQGTCLKAKNEFKKRCQLQATITQDSTYGDEDC 100

101 LYLNIWVPQGRKQVSRDLPVMIWIYGAFLMGSGHGANFLNNLYDGEI 150
   |||||
101 LYLNIWVPQGRKQVSRDLPVMIWIYGAFLMGSGHGANFLNNLYDGEI 150

151 ATRGNVIVVTENYRVGPLGFLSTGDANLPGNYGLRDQHMAIAWVKRNIAA 200
   |||||
151 ATRGNVIVVTENYRVGPLGFLSTGDANLPGNYGLRDQHMAIAWVKRNIAA 200

201 FGGDPNNITLFGESAGGASVSLQTLSPYNKGLIRRAISQSGVALSPWVIQ 250
   |||||
201 FGGDPNNITLFGESAGGASVSLQTLSPYNKGLIRRAISQSGVALSPWVIQ 250

```

Fig. 18

Fig. 18 (Cont.¹).

501 DSAVPTHWEPTYTENS GYLEITKKMGSSMKRSLRTNFLRYWTLTYLALP 550
|||||
501 DSAVPTHWEPTYTENS GYLEITKKMGSSMKRSLRTNFLRYWTLTYLALP 550
551 TVTDQEATPVPPPTG DSEATPVPPPTG DSEATPVPPPTG DSGAPPVPPTG DSG 600
|||||
551 TVTDQEATPVPPPTG DSEATPVPPPTG DSEATPVPPPTG DSGAPPVPPTG DSG 600
601 APPVPPTG DSGAPPVPPTG DSGAPPVPPTG DSGAPPVP 639
|||||
601 APPVPPTG DSGAPPVPPTG DSGAPPVPPTG DSGAPPVP 639

Fig. 18 (Cont.²)

1 MRALLARLLLCVLVSDSKGSNELHQVPSNCDCLNGGTCVSNKYFSNIHW 50
|||||
1 MRALLARLLLCVLVSDSKGSNELHQVPSNCDCLNGGTCVSNKYFSNIHW 50
51 CNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVL 100
|||||
51 CNCPKKFGGQHCEIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVL 100
101 QQTYHAHRSDALQLGLGKHNYCR 123
|||||
101 QQTYHAHRSDALQLGLGKHNYCR 123

Fig. 19

1 MKTYRAKFCGVCTDGRCCCTPHRTTTLPVEFKCPDGEVMKKNNMMFIKTCAC 50
|||||
276 MKTYRAKFCGVCTDGRCCCTPHRTTTLPVEFKCPDGEVMKKNNMMFIKTCAC 325

51 HYNCPGDNDIFESLYYRKMYGDMA 74
|||||
326 HYNCPGDNDIFESLYYRKMYGDMA 349

Fig. 20

1 MTAASMGPVRAFVLLALCSRPAVGQNCSGPCRCPDEPAPRCPAGVSLV 50
|||||
1 MTAASMGPVRAFVLLALCSRPAVGQNCSGPCRCPDEPAPRCPAGVSLV 50
51 LDGCGCCRVCAKQLGELCTERDPCDPHKGLECFDGFSPANRKIGVCTAKDG 100
|||||
51 LDGCGCCRVCAKQLGELCTERDPCDPHKGLECFDGFSPANRKIGVCTAKDG 100
101 APCIFGGTVYRSGESFQSSCKYQCTCLDGAVGCMPLCSMDVRLPSPDCPF 150
|||||
101 APCIFGGTVYRSGESFQSSCKYQCTCLDGAVGCMPLCSMDVRLPSPDCPF 150

151 P 151

151 P 151

Fig. 21

1 MENSRLCVWVPKLAFLFGASLLSAHLQVTGFQIKAFALRFLSEPSDAV 50
|||||
1 MENSRLCVWVPKLAFLFGASLLSAHLQVTGFQIKAFALRFLSEPSDAV 50
.
51 TMRGGNVLLDCSAESDRGVPVIKWKDCIHLALGMDERKQQLSNGSLLIQ 100
|||||
51 TMRGGNVLLDCSAESDRGVPVIKWKDCIHLALGMDERKQQLSNGSLLIQ 100
.
101 NILHSRHHKPDGLYQCEASLGDSGSIISRTAKVAVAGP 139
|||||
101 NILHSRHHKPDGLYQCEASLGDSGSIISRTAKVAVAGP 139

Fig. 22

```

1 MAPFEPLASGILLLLWLIAPSRACVCVPPHPQTAFCNSDLVIRAKFVGTP 50
  |||||
1 MAPFEPLASGILLLLWLIAPSRACVCVPPHPQTAFCNSDLVIRAKFVGTP 50

51 EVNQTTLYQRYEIKMTKMYKGFOALXDAADIRFVYTPAMESVCCGYFHRSH 100
  |||||
51 EVNQTTLYQRYEIKMTKMYKGFOALGDAADIRFVYTPAMESVCCGYFHRSH 100

101 NRS 103
  |||
101 NRS 103

```

Fig. 23

Fig. 25

1 MTKMYKGEQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLLIAGKLQD 50
|||||
65 MTKMYKGEQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLLIAGKLQD 114
51 GLLHITTCFVAPWNLSLAQRRGFTKTYTVGCCECTVFPCLSI PCKLQS 100
|||||
115 GLLHITTCFVAPWNLSLAQRRGFTKTYTVGCCECTVFPCLSI PCKLQS 164
101 GTHCLWTDQLLQSEKGFQSRHLACLPREPGLCTWQSLRSQIA 143
|||||
165 GTHCLWTDQLLQSEKGFQSRHLACLPREPGLCTWQSLRSQIA 207

Fig. 26